

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ruben, Steven M
- (ii) TITLE OF INVENTION: Apoptosis Inducing Molecule I
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Human Genome Sciences, Inc.
 - (B) STREET: 9410 Key West Avenue
 - (C) CITY: Rockville
 - (D) STATE: MD
 - (E) COUNTRY: US
 - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 13-MAR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kimball, Paul, C.
 - (B) REGISTRATION NUMBER: 34,610
 - (C) REFERENCE/DOCKET NUMBER: PF261
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (301) 309-8504
 - (B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 52..894
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGCG GCTGCCTGGC TGA CTTACAG CAGTCAGACT CTGACAGGTT C ATG GCT
Met Ala
1

57

ATG	ATG	GAG	GTC	CAG	GGG	GGA	CCC	AGC	CTG	GGA	CAG	ACC	TGC	GTG	CTG	105
Met	Met	Glu	Val	Gln	Gly	Gly	Pro	Ser	Leu	Gly	Gln	Thr	Cys	Val	Leu	
		5					10					15				
ATC	GTG	ATC	TTC	ACA	GTG	CTC	CTG	CAG	TCT	CTC	TGT	GTG	GCT	GTA	ACT	153
Ile	Val	Ile	Phe	Thr	Val	Leu	Leu	Gln	Ser	Leu	Cys	Val	Ala	Val	Thr	
	20					25					30					
TAC	GTG	TAC	TTT	ACC	AAC	GAG	CTG	AAG	CAG	ATG	CAG	GAC	AAG	TAC	TCC	201
Tyr	Val	Tyr	Phe	Thr	Asn	Glu	Leu	Lys	Gln	Met	Gln	Asp	Lys	Tyr	Ser	
	35				40					45					50	
AAA	AGT	GGC	ATT	GCT	TGT	TTC	TTA	AAA	GAA	GAT	GAC	AGT	TAT	TGG	GAC	249
Lys	Ser	Gly	Ile	Ala	Cys	Phe	Leu	Lys	Glu	Asp	Asp	Ser	Tyr	Trp	Asp	
				55					60					65		
CCC	AAT	GAC	GAA	GAG	AGT	ATG	AAC	AGC	CCC	TGC	TGG	CAA	GTC	AAG	TGG	297
Pro	Asn	Asp	Glu	Glu	Ser	Met	Asn	Ser	Pro	Cys	Trp	Gln	Val	Lys	Trp	
			70					75					80			
CAA	CTC	CGT	CAG	CTC	GTT	AGA	AAG	ATG	ATT	TTG	AGA	ACC	TCT	GAG	GAA	345
Gln	Leu	Arg	Gln	Leu	Val	Arg	Lys	Met	Ile	Leu	Arg	Thr	Ser	Glu	Glu	
		85					90					95				
ACC	ATT	TCT	ACA	GTT	CAA	GAA	AAG	CAA	CAA	AAT	ATT	TCT	CCC	CTA	GTG	393
Thr	Ile	Ser	Thr	Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile	Ser	Pro	Leu	Val	
	100					105					110					
AGA	GAA	AGA	GGT	CCT	CAG	AGA	GTA	GCA	GCT	CAC	ATA	ACT	GGG	ACC	AGA	441
Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	
	115				120				125						130	
GGA	AGA	AGC	AAC	ACA	TTG	TCT	TCT	CCA	AAC	TCC	AAG	AAT	GAA	AAG	GCT	489
Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	Ala	
				135				140					145			
CTG	GGC	CGC	AAA	ATA	AAC	TCC	TGG	GAA	TCA	TCA	AGG	AGT	GGG	CAT	TCA	537
Leu	Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser	Ser	Arg	Ser	Gly	His	Ser	
			150					155					160			
TTC	CTG	AGC	AAC	TTG	CAC	TTG	AGG	AAT	GGT	GAA	CTG	GTC	ATC	CAT	GAA	585
Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val	Ile	His	Glu	
		165					170					175				
AAA	GGG	TTT	TAC	TAC	ATC	TAT	TCC	CAA	ACA	TAC	TTT	CGA	TTT	CAG	GAG	633
Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg	Phe	Gln	Glu	
	180					185					190					
GAA	ATA	AAA	GAA	AAC	ACA	AAG	AAC	GAC	AAA	CAA	ATG	GTC	CAA	TAT	ATT	681
Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val	Gln	Tyr	Ile	
	195				200				205						210	
TAC	AAA	TAC	ACA	AGT	TAT	CCT	GAC	CCT	ATA	TTG	TTG	ATG	AAA	AGT	GCT	729
Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met	Lys	Ser	Ala	
				215				220					225			
AGA	AAT	AGT	TGT	TGG	TCT	AAA	GAT	GCA	GAA	TAT	GGA	CTC	TAT	TCC	ATC	777
Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	Ile	
			230					235				240				

TAT CAA GGG GGA ATA TTT GAG CTT AAG GAA AAT GAC AGA ATT TTT GTT	825
Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val	
245 250 255	
TCT GTA ACA AAT GAG CAC TTG ATA GAC ATG GAC CAT GAA GCC AGT TTT	873
Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe	
260 265 270	
TTC GGG GCC TTT TTA GTT GGC TAACTGACCT GGAAAGAAAA AGCAATAACC	924
Phe Gly Ala Phe Leu Val Gly	
275 280	
TCAAAGTGAC TATTCAGTTT TCAGGATGAT ACACTATGAA GATGTTTCAA AAAATCTGAC	984
CAAAACAAAC AAACAGAAAA CAGAAAACAA AAAAACCTCT ATGCAATCTG AGTAGAGCAG	1044
CCACAACCAA AAAATTCTAC AACACACACT GTTCTGAAAG TGACTCACTT ATCCCAAGAA	1104
AATGAAATTG CTGAAAGATC TTTCAGGACT CTACCTCATA TCAGTTTGCT AGCAGAAATC	1164
TAGAAGACTG TCAGCTTCCA AACATTAATG CAATGGTTAA CATCTTCTGT CTTTATAATC	1224
TACTCCTTGT AAAGACTGTA GAAGAAAGCG CAACAATCCA TCTCTCAAGT AGTGTATCAC	1284
AGTAGTAGCC TCCAGGTTTC CTTAAGGGAC AACATCCTTA AGTCAAAAGA GAGAAGAGGC	1344
ACCACTAAAA GATCGCAGTT TGCCTGGTGC AGTGGCTCAC ACCTGTAATC CCAACATTTT	1404
GGGAACCCAA GGTGGGTAGA TCACGAGATC AAGAGATCAA GACCATAGTG ACCAACATAG	1464
TGAAACCCCA TCTCTACTGA AAGTGCAAAA ATTAGCTGGG TGTGTTGGCA CATGCCTGTA	1524
GTCCCAGCTA CTTGAGAGGC TGAGGCAGGA GAATCGTTTG AACCCGGGAG GCAGAGGTTG	1584
CAGTGTGGTG AGATCATGCC ACTACACTCC AGCCTGGCGA CAGAGCGAGA CTTGGTTTC	1643

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
1 5 10 15
Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
20 25 30
Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
35 40 45
Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
50 55 60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
 65 70 75 80
 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
 85 90 95
 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
 100 105 110
 Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
 115 120 125
 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
 130 135 140
 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
 145 150 155 160
 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
 165 170 175
 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
 180 185 190
 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
 195 200 205
 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
 210 215 220
 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
 225 230 235 240
 Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
 245 250 255
 Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
 260 265 270
 Ser Phe Phe Gly Ala Phe Leu Val Gly
 275 280

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Asp Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu
 1 5 10 15

Pro	Cys	Pro	Thr	Ser	Val	Pro	Arg	Arg	Pro	Gly	Gln	Arg	Arg	Pro	Pro		
			20					25					30				
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro		
		35					40					45					
Leu	Pro	Pro	Leu	Pro	Leu	Pro	Pro	Leu	Lys	Lys	Arg	Gly	Asn	His	Ser		
	50					55					60						
Thr	Gly	Leu	Cys	Leu	Leu	Val	Met	Phe	Phe	Met	Val	Leu	Val	Ala	Leu		
65					70					75					80		
Val	Gly	Leu	Gly	Leu	Gly	Met	Phe	Gln	Leu	Phe	His	Leu	Gln	Lys	Glu		
				85					90					95			
Leu	Ala	Glu	Leu	Arg	Glu	Ser	Thr	Ser	Gln	Met	His	Thr	Ala	Ser	Ser		
			100					105					110				
Leu	Glu	Lys	Gln	Ile	Gly	His	Pro	Ser	Pro	Pro	Pro	Glu	Lys	Lys	Glu		
		115					120					125					
Leu	Arg	Lys	Val	Ala	His	Leu	Thr	Gly	Lys	Ser	Asn	Ser	Arg	Ser	Met		
	130					135					140						
Pro	Leu	Glu	Trp	Glu	Asp	Thr	Tyr	Gly	Ile	Val	Leu	Leu	Ser	Gly	Val		
145					150					155					160		
Lys	Tyr	Lys	Lys	Gly	Gly	Leu	Val	Ile	Asn	Glu	Thr	Gly	Leu	Tyr	Phe		
				165					170					175			
Val	Tyr	Ser	Lys	Val	Tyr	Phe	Arg	Gly	Gln	Ser	Cys	Asn	Asn	Leu	Pro		
			180					185					190				
Leu	Ser	His	Lys	Val	Tyr	Met	Arg	Asn	Ser	Lys	Tyr	Pro	Gln	Asp	Leu		
		195					200					205					
Val	Met	Met	Glu	Gly	Lys	Met	Met	Ser	Tyr	Cys	Thr	Thr	Gly	Gln	Met		
	210					215					220						
Trp	Ala	Arg	Ser	Ser	Tyr	Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr	Ser	Ala		
225					230					235					240		
Asp	His	Leu	Tyr	Val	Asn	Val	Ser	Glu	Leu	Ser	Leu	Val	Asn	Phe	Glu		
				245					250					255			
Glu	Ser	Gln	Thr	Phe	Phe	Gly	Leu	Tyr	Lys	Leu							
			260					265									

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gln	Gln	Pro	Met	Asn	Tyr	Pro	Cys	Pro	Gln	Ile	Phe	Trp	Val	Asp	
1				5					10					15		
Ser	Ser	Ala	Thr	Ser	Ser	Trp	Ala	Pro	Pro	Gly	Ser	Val	Phe	Pro	Cys	
			20					25					30			
Pro	Ser	Cys	Gly	Pro	Arg	Gly	Pro	Asp	Gln	Arg	Arg	Pro	Pro	Pro	Pro	
		35					40					45				
Pro	Pro	Pro	Val	Ser	Pro	Leu	Pro	Pro	Pro	Ser	Gln	Pro	Leu	Pro	Leu	
	50					55					60					
Pro	Pro	Leu	Thr	Pro	Leu	Lys	Lys	Lys	Asp	His	Asn	Thr	Asn	Leu	Trp	
65					70					75					80	
Leu	Pro	Val	Val	Phe	Phe	Met	Val	Leu	Val	Ala	Leu	Val	Gly	Met	Gly	
				85					90					95		
Leu	Gly	Met	Tyr	Gln	Leu	Phe	His	Leu	Gln	Lys	Glu	Leu	Ala	Glu	Leu	
			100					105					110			
Arg	Glu	Phe	Thr	Asn	Gln	Ser	Leu	Lys	Val	Ser	Ser	Phe	Glu	Lys	Gln	
		115					120					125				
Ile	Ala	Asn	Pro	Ser	Thr	Pro	Ser	Glu	Lys	Lys	Glu	Pro	Arg	Ser	Val	
	130					135					140					
Ala	His	Leu	Thr	Gly	Asn	Pro	His	Ser	Arg	Ser	Ile	Pro	Leu	Glu	Trp	
145					150					155					160	
Glu	Asp	Thr	Tyr	Gly	Thr	Ala	Leu	Ile	Ser	Gly	Val	Lys	Tyr	Lys	Lys	
				165					170					175		
Gly	Gly	Leu	Val	Ile	His	Glu	Thr	Gly	Leu	Tyr	Phe	Val	Tyr	Ser	Lys	
			180					185					190			
Val	Tyr	Phe	Arg	Gly	Gln	Ser	Cys	Asn	Asn	Gln	Pro	Leu	Asn	His	Lys	
		195					200					205				
Val	Tyr	Met	Arg	Asn	Ser	Lys	Tyr	Pro	Glu	Asp	Leu	Val	Leu	Met	Glu	
	210					215					220					
Glu	Lys	Arg	Leu	Asn	Tyr	Cys	Thr	Thr	Gly	Gln	Ile	Trp	Ala	His	Ser	
225					230					235					240	
Ser	Tyr	Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr	Ser	Ala	Asp	His	Leu	Tyr	
				245					250					255		
Val	Asn	Ile	Ser	Gln	Leu	Ser	Leu	Ile	Asn	Phe	Glu	Glu	Ser	Lys	Thr	
				260				265					270			
Phe	Phe	Gly	Leu	Tyr	Lys	Leu										
			275													

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ser	Thr	Glu	Ser	Met	Ile	Arg	Asp	Val	Glu	Leu	Ala	Glu	Glu	Ala	1	5	10	15
Leu	Pro	Lys	Lys	Thr	Gly	Gly	Pro	Gln	Gly	Ser	Arg	Arg	Cys	Leu	Phe	20	25	30	
Leu	Ser	Leu	Phe	Ser	Phe	Leu	Ile	Val	Ala	Gly	Ala	Thr	Thr	Leu	Phe	35	40	45	
Cys	Leu	Leu	His	Phe	Gly	Val	Ile	Gly	Pro	Gln	Arg	Glu	Glu	Ser	Pro	50	55	60	
Arg	Asp	Leu	Ser	Leu	Ile	Ser	Pro	Leu	Ala	Gln	Ala	Val	Arg	Ser	Ser	65	70	75	80
Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro	85	90	95	
Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu	100	105	110	
Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser	115	120	125	
Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly	130	135	140	
Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala	145	150	155	160
Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys	Ser	Pro	165	170	175	
Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr	Glu	180	185	190	
Pro	Ile	Tyr	Leu	Gly	Cys	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg	Leu	195	200	205	
Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe	Ala	Glu	Ser	Gly	210	215	220	
Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	225	230									

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
1           5           10           15

Leu His Leu Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
          20           25           30

Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala
          35           40           45

Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
          50           55           60

Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
65           70           75           80

Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
          85           90           95

Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
          100          105          110

Val Val Phe Ser Cys Lys Ala Tyr Ser Pro Lys Ala Pro Ser Ser Pro
          115          120          125

Leu Tyr Leu Ala His Glu Val Cys Leu Phe Ser Ser Gln Tyr Pro Phe
          130          135          140

His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
          145          150          155          160

Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
          165          170          175

Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
          180          185          190

Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
          195          200          205

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCGGGAT CCATGGCTAT GATGGAGGTC CAG

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGCGTCTA GAGCTTAGGC AACTAAAAAG GCC

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGCGCGGAT CCATCATGGC TATGATGGAG GTCC

34

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGCGTCTA GAGCTTAGCC AACTAAAAAG GCC

33